

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 12:13:19 ; Search time 161 Seconds

(Without alignments)
40.793 Million cell updates/sec

Title: US-09-647-457E-1

Perfect score: 83

Sequence: 1 LVVGLCTGKIKTGAPAC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US10A_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubppa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1 | 76 | 91.6 | 458 | US-10-733-969A-13 | Sequence 13, Appl |
| 2 | 76 | 91.6 | 458 | US-10-478-519-6 | Sequence 6, Appl |
| 3 | 67 | 80.7 | 50 | US-10-776-013-325 | Sequence 325, App |
| 4 | 67 | 80.7 | 269 | US-10-473-127-1043 | Sequence 1043, App |
| 5 | 67 | 80.7 | 272 | US-10-473-127-1041 | Sequence 1041, App |
| 6 | 67 | 80.7 | 272 | US-10-473-127-1044 | Sequence 1044, App |
| 7 | 67 | 80.7 | 336 | US-10-473-127-1042 | Sequence 1042, App |
| 8 | 67 | 80.7 | 420 | US-10-498-788-17 | Sequence 17, Appl |
| 9 | 67 | 80.7 | 429 | US-10-473-127-604 | Sequence 604, App |
| 10 | 67 | 80.7 | 433 | US-09-935-642-9 | Sequence 9, Appl |
| 11 | 67 | 80.7 | 433 | US-10-733-969A-61 | Sequence 61, Appl |

| | | | | | | |
|----|----|------|-----|----|----------------------|----------------------|
| 12 | 67 | 80.7 | 433 | 16 | US-10-473-127-608 | Sequence 608, App |
| 13 | 67 | 80.7 | 433 | 16 | US-10-473-127-610 | Sequence 610, App |
| 14 | 67 | 80.7 | 434 | 14 | US-10-177-293-124 | Sequence 124, App |
| 15 | 67 | 80.7 | 434 | 14 | US-10-205-194-47 | Sequence 47, Appl |
| 16 | 67 | 80.7 | 434 | 14 | US-10-354-358-16 | Sequence 16, Appl |
| 17 | 67 | 80.7 | 434 | 15 | US-10-170-385-257 | Sequence 257, App |
| 18 | 67 | 80.7 | 434 | 15 | US-10-170-385-273 | Sequence 273, App |
| 19 | 67 | 80.7 | 434 | 15 | US-10-258-666-10 | Sequence 10, Appl |
| 20 | 67 | 80.7 | 434 | 15 | US-10-205-331-26 | Sequence 26, Appl |
| 21 | 67 | 80.7 | 434 | 16 | US-10-473-127-595 | Sequence 595, App |
| 22 | 67 | 80.7 | 434 | 16 | US-10-473-127-596 | Sequence 596, App |
| 23 | 67 | 80.7 | 434 | 16 | US-10-473-127-597 | Sequence 597, App |
| 24 | 67 | 80.7 | 434 | 16 | US-10-473-127-598 | Sequence 598, App |
| 25 | 67 | 80.7 | 434 | 16 | US-10-473-127-599 | Sequence 599, App |
| 26 | 67 | 80.7 | 434 | 16 | US-10-473-127-600 | Sequence 600, App |
| 27 | 67 | 80.7 | 434 | 16 | US-10-473-127-601 | Sequence 601, App |
| 28 | 67 | 80.7 | 434 | 16 | US-10-473-127-602 | Sequence 602, App |
| 29 | 67 | 80.7 | 434 | 16 | US-10-473-127-603 | Sequence 603, App |
| 30 | 67 | 80.7 | 434 | 16 | US-10-473-127-609 | Sequence 609, App |
| 31 | 67 | 80.7 | 434 | 16 | US-10-723-860-117 | Sequence 117, App |
| 32 | 67 | 80.7 | 434 | 16 | US-10-723-860-1948 | Sequence 1948, App |
| 33 | 67 | 80.7 | 434 | 16 | US-10-370-715B-38 | Sequence 38, Appl |
| 34 | 67 | 80.7 | 434 | 16 | US-10-873-595-15 | Sequence 15, Appl |
| 35 | 67 | 80.7 | 434 | 17 | US-10-489-740-146 | Sequence 146, App |
| 36 | 67 | 80.7 | 434 | 18 | US-10-491-545A-36 | Sequence 36, Appl |
| 37 | 67 | 80.7 | 434 | 18 | US-10-676-691-13 | Sequence 13, Appl |
| 38 | 67 | 80.7 | 434 | 18 | US-10-676-691-15 | Sequence 15, Appl |
| 39 | 67 | 80.7 | 434 | 18 | US-10-676-691-21 | Sequence 21, Appl |
| 40 | 67 | 80.7 | 434 | 18 | US-10-676-691-22 | Sequence 22, Appl |
| 41 | 67 | 80.7 | 434 | 18 | US-10-676-691-23 | Sequence 23, Appl |
| 42 | 61 | 73.5 | 434 | 18 | US-10-676-691-23 | Sequence 24, Appl |
| 43 | 58 | 69.9 | 163 | 16 | US-10-767-701-55929 | Sequence 55929, App |
| 44 | 58 | 69.9 | 434 | 15 | US-10-369-493-5507 | Sequence 5507, App |
| 45 | 54 | 65.1 | 112 | 16 | US-10-437-963-192587 | Sequence 192587, App |

ALIGNMENTS

RESULT 1
US-10-733-969A-13
; Sequence 13, Application US/10733969A
; Publication No. US20040219572A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, JIE
; APPLICANT: HU, LIPING
; APPLICANT: LIU, TONG HUA
; APPLICANT: LU, ZHAO HUI
; APPLICANT: SHEN, YAN
; TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCRATIC CANCER
; FILE REFERENCE: 21525
; CURRENT APPLICATION NUMBER: US/10/733,969A
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 02028058.2
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 13
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Alpha enolase; Accession NO: as of 06 Dec 2002: Q05524
US-10-733-969A-13

Query Match 91.6%; Score 76; DB 16; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.0008; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 LVVGLCTGKIKTGAPAC 16
|||||
DB 407 LVVGLCTGKIKTGAPAC 422

```
RESULT 2
US-10-478-519-6
; Sequence 6, Application US/10478519
; Publication No. US2005042738A1
; GENERAL INFORMATION:
; APPLICANT: SWARNAKAR, Anita; GORVAD, Ann E.;
; APPLICANT: HAFALIA, April J.A.; DUGGAN, Brendan M.;
; APPLICANT: EMERLING, Brooke M.; ISON, Craig H.;
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
; APPLICANT: YUE, Henry; YUE, Hubin;
; APPLICANT: FORSTHER, Ian J.; LI, Joana X.;
; APPLICANT: THANGAVELOU, Kavitha; CHAMLA, Nandinder K.;
; APPLICANT: BURFORD, Neil; MASON, Patricia M.;
; APPLICANT: LAL, Preeti G.; LEE, Sally;
; APPLICANT: BECHA, Shanya D.; TANG, Y. Tom
; TITLE OF INVENTION: Carbohydrate-Associated Proteins
; FILE REFERENCE: PF-0982 USN
; CURRENT APPLICATION NUMBER: US/10/478,519
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/18354
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293,768
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/309,548
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/314,400
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 60/343,706
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/337,999
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inocyte ID No: 7488348CD1
US-10-478-519-6

Query Match          91.6%; Score 76; DB 17; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.0008;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 LVVGLCTQIKTGAPC 16
        |||||
Db      407 LVVGLCTGQIKTGPTC 422

RESULT 3
US-10-776-013-325
; Sequence 325, Application US/10776013
; Publication No. US20040226056A1
; GENERAL INFORMATION:
; APPLICANT: MYRIAD GENETICS, INC.
; APPLICANT: ROCH, Jean-Marc
; APPLICANT: BARTEL, Paul
; APPLICANT: HEICHMAN, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776,013
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
```

```
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 325
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-013-325

Query Match          80.7%; Score 67; DB 16; Length 50;
Best Local Similarity 81.2%; Pred. No. 0.0027;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTQIKTGAPC 16
        |||||
Db      24 LVVGLCTGQIKTGAPC 39

RESULT 4
US-10-473-127-1043
; Sequence 1043, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: ZYCOS INC.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1043
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1043

Query Match          80.7%; Score 67; DB 16; Length 269;
Best Local Similarity 81.2%; Pred. No. 0.013;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTQIKTGAPC 16
        |||||
Db      219 LVVGLCTGQIKTGAPC 234

RESULT 5
US-10-473-127-1041
; Sequence 1041, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: ZYCOS INC.
```

```

; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1041
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1041
```

```

Query Match      80.7%; Score 67; DB 16; Length 272;
Best Local Similarity 81.2%; Pred. No. 0.013;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTGXIKTGAPC 16
Db      222 LVVGLCTGXIKTGAPC 237
```

```

RESULT 6
US-10-473-127-1044
; Sequence 1044, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1044
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1044
```

```

Query Match      80.7%; Score 67; DB 16; Length 272;
Best Local Similarity 81.2%; Pred. No. 0.013;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTGXIKTGAPC 16
Db      222 LVVGLCTGXIKTGAPC 237
```

RESULT 7

```

US-10-473-127-1042
; Sequence 1042, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1042
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1042
```

```

Query Match      80.7%; Score 67; DB 16; Length 336;
Best Local Similarity 81.2%; Pred. No. 0.016;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTGXIKTGAPC 16
Db      286 LVVGLCTGXIKTGAPC 301
```

```

RESULT 8
US-10-498-788-17
; Sequence 17, Application US/10498788
; Publication No. US20050118594A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: Chawla, Nandinder K.
; APPLICANT: Lee, Soo Yeun
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Lee, Ernestine A.
; APPLICANT: Forsythe, Ian J.
; APPLICANT: Khare, Keena
; APPLICANT: Tran, Uyen K.
; APPLICANT: Kable, Amy E.
; APPLICANT: Richardson, Thomas W.
; APPLICANT: Emerling, Brooke M.
; APPLICANT: Lindquist, Erika A.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Hatalia, April J. A.
; APPLICANT: Jin, Pei
; APPLICANT: Swarnakar, Anita
; APPLICANT: Li, Joana X.
; APPLICANT: Margrie, Joseph P.
; APPLICANT: Lee, Sally
; APPLICANT: Gorvad, Ann E.
; APPLICANT: Sprague, William W.
; APPLICANT: Becha, Shanya D.
; APPLICANT: Elliott, Vicki S.
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: PF-1312 PCT
; CURRENT APPLICATION NUMBER: US/10/498,788
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/340,357
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/342,962
```

```
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: US 60/343,558
/ PRIOR FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: US 60/351,107
/ PRIOR FILING DATE: 2002-01-22
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: PERL Program
/ SEQ ID NO 17
/ LENGTH: 420
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No: 7506054CD1
US-10-498-788-17
```

```
Query Match      80.7%; Score 67; DB 17; Length 420;
Best Local Similarity 81.2%; Pred. No. 0.02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTQXQIKTGAPC 16
Db      370 LVVGLCTGQIKTGAPC 385
```

```
RESULT 9
US-10-473-127-604
```

```
/ Sequence 604, Application US/10473127
/ Publication No. US20040236091A1
/ GENERAL INFORMATION:
/ APPLICANT: Zycos Inc.
/ TITLE OF INVENTION: TRANSLATIONAL PROFILING
/ FILE REFERENCE: 08191-026W01
/ CURRENT APPLICATION NUMBER: US/10/473,127
/ CURRENT FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: 60/279,495
/ PRIOR FILING DATE: 2001-03-28
/ PRIOR APPLICATION NUMBER: 60/292,544
/ PRIOR FILING DATE: 2001-05-21
/ PRIOR APPLICATION NUMBER: 60/310,801
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: 60/326,370
/ PRIOR FILING DATE: 2001-10-01
/ PRIOR APPLICATION NUMBER: 60/336,780
/ PRIOR FILING DATE: 2001-12-04
/ PRIOR APPLICATION NUMBER: 60/358,985
/ PRIOR FILING DATE: 2002-02-20
/ NUMBER OF SEQ ID NOS: 2041
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 604
/ LENGTH: 429
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-473-127-604
```

```
Query Match      80.7%; Score 67; DB 16; Length 429;
Best Local Similarity 81.2%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTQXQIKTGAPC 16
Db      379 LVVGLCTGQIKTGAPC 394
```

```
RESULT 10
US-09-935-642-9
```

```
/ Sequence 9, Application US/09935642
/ Publication No. US20030044795A1
/ GENERAL INFORMATION:
/ APPLICANT: BYRJALSEN, Inger
/ APPLICANT: LARSEN, Peter
/ APPLICANT: STEPHEN, John
/ TITLE OF INVENTION: Biochemical Markers for the Human
```

```
/ TITLE OF INVENTION: Endometrium
/ FILE REFERENCE: 8969-014
/ CURRENT APPLICATION NUMBER: US/09/935,642
/ CURRENT FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: PCT/GB97/02394
/ PRIOR FILING DATE: 1997-09-05
/ PRIOR APPLICATION NUMBER: PCT/GB9707132.8
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: PCT/GB9618600.2
/ PRIOR FILING DATE: 1996-09-06
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 433
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-935-642-9
```

```
Query Match      80.7%; Score 67; DB 10; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTQXQIKTGAPC 16
Db      383 LVVGLCTGQIKTGAPC 398
```

```
RESULT 11
US-10-733-969A-61
```

```
/ Sequence 61, Application US/10733969A
/ Publication No. US20040219572A1
/ GENERAL INFORMATION:
/ APPLICANT: CHEN, JIE
/ APPLICANT: HU, LIPING
/ APPLICANT: LIU, TONG HUA
/ APPLICANT: LU, ZHAO HUI
/ APPLICANT: SHEN, YAN
/ TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCREATIC CANCER
/ FILE REFERENCE: 21525
/ CURRENT APPLICATION NUMBER: US/10/733,969A
/ CURRENT FILING DATE: 2003-12-11
/ PRIOR APPLICATION NUMBER: EP 02028058.2
/ PRIOR FILING DATE: 2002-12-17
/ NUMBER OF SEQ ID NOS: 110
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 61
/ LENGTH: 433
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human alpha enolase; Accession NO:
/ OTHER INFORMATION: as of 29 August 2003: P06733
US-10-733-969A-61
```

```
Query Match      80.7%; Score 67; DB 16; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTQXQIKTGAPC 16
Db      383 LVVGLCTGQIKTGAPC 398
```

```
RESULT 12
US-10-473-127-608
```

```
/ Sequence 608, Application US/10473127
/ Publication No. US20040236091A1
/ GENERAL INFORMATION:
/ APPLICANT: Zycos Inc.
/ TITLE OF INVENTION: TRANSLATIONAL PROFILING
/ FILE REFERENCE: 08191-026W01
/ CURRENT APPLICATION NUMBER: US/10/473,127
/ CURRENT FILING DATE: 2003-09-26
```

```

; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 608
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-608

Query Match      80.7%; Score 67; DB 16; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTGXQIKTGAPC 16
DB      383 LVVGLCTGXQIKTGAPC 398

RESULT 13
US-10-473-127-610
; Sequence 610, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026M01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 610
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-610

Query Match      80.7%; Score 67; DB 16; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTGXQIKTGAPC 16
DB      383 LVVGLCTGXQIKTGAPC 398

RESULT 14
US-10-177-293-124
; Sequence 124, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lilly, James
; APPLICANT: Glatic, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Ganavaypu, Manjula
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vile
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Best Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puzstai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; PRIOR FILING DATE: 2002-06-21
; CURRENT APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-124

Query Match      80.7%; Score 67; DB 14; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTGXQIKTGAPC 16
DB      384 LVVGLCTGXQIKTGAPC 399

RESULT 15
US-10-205-194-47
; Sequence 47, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alister
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pimock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; PRIOR FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 434
; TYPE: PRT
```

;
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Neuron-specific enolase
US-10-205-194-47

Query Match 80.7%; Score 67; DB 14; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTXQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399

Search completed: July 13, 2005, 12:26:54
Job time : 162 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 12:03:53 ; Search time 56 Seconds
(Without alignments) 155.453 Million cell updates/sec

Title: US-09-647-457E-1

Perfect score: 83

Sequence: 1 LVVGLCTKXIKTGPACX 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

1612378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 76 | 91.6 | 458 | 1 ENOA_HUMAN | Q05524 homo sapien |
| 2 | 70 | 84.3 | 433 | 1 ENOA_BOVIN | Q9XJ44 bos taurus |
| 3 | 67 | 80.7 | 88 | 2 Q804Y6 | Q804Y6 ictalurus p |
| 4 | 67 | 80.7 | 154 | 2 Q9NPL4 | Q9NPL4 homo sapien |
| 5 | 67 | 80.7 | 159 | 2 Q9NG70 | Q9NG70 peripatus s |
| 6 | 67 | 80.7 | 184 | 2 Q9GCV1 | Q9GCV1 homo sapien |
| 7 | 67 | 80.7 | 259 | 2 Q7ZZM5 | Q7ZZM5 sparus aura |
| 8 | 67 | 80.7 | 264 | 2 Q8WU71 | Q8WU71 homo sapien |
| 9 | 67 | 80.7 | 272 | 2 Q9BR62 | Q9BR62 homo sapien |
| 10 | 67 | 80.7 | 336 | 2 Q71V37 | Q71V37 homo sapien |
| 11 | 67 | 80.7 | 338 | 2 Q922A0 | Q922A0 homo sapien |
| 12 | 67 | 80.7 | 341 | 2 Q6GMP2 | Q6GMP2 homo sapien |
| 13 | 67 | 80.7 | 353 | 2 Q99KT7 | Q99KT7 mus musculu |
| 14 | 67 | 80.7 | 366 | 2 Q6PHC1 | Q6PHC1 mus musculu |
| 15 | 67 | 80.7 | 374 | 2 Q658M5 | Q658M5 homo sapien |
| 16 | 67 | 80.7 | 377 | 2 Q6LDP3 | Q6LDP3 anas platyr |
| 17 | 67 | 80.7 | 383 | 2 Q9NG67 | Q9NG67 tomocerus s |
| 18 | 67 | 80.7 | 394 | 2 Q9PTX6 | Q9PTX6 lampetra re |
| 19 | 67 | 80.7 | 395 | 1 ENO_ALAMI | P42897 alligator m |
| 20 | 67 | 80.7 | 395 | 2 Q9PTX5 | Q9PTX5 lampetra re |
| 21 | 67 | 80.7 | 395 | 2 Q9USF7 | Q9USF7 eptaretus |
| 22 | 67 | 80.7 | 432 | 2 Q61QPS | Q61QPS brachydantio |
| 23 | 67 | 80.7 | 432 | 2 Q6PC12 | Q6PC12 brachydantio |
| 24 | 67 | 80.7 | 433 | 1 ENOA_ALAMI | Q9PK22 alligator m |
| 25 | 67 | 80.7 | 433 | 1 ENOA_ANAPL | P19140 anas platyr |
| 26 | 67 | 80.7 | 433 | 1 ENOA_CHICK | P51913 gallus gall |
| 27 | 67 | 80.7 | 433 | 1 ENOA_HUMAN | P06733 gallus gall |
| 28 | 67 | 80.7 | 433 | 1 ENOA_MOUSE | P17182 mus musculu |
| 29 | 67 | 80.7 | 433 | 1 ENOA_PYTRG | Q9W710 python regi |
| 30 | 67 | 80.7 | 433 | 1 ENOA_RAT | P04764 rattus norv |
| 31 | 67 | 80.7 | 433 | 1 ENOA_SCEUN | Q9W712 sceloporus |

ALIGNMENTS

| | | | | | |
|----|----|------|-----|--------------|---------------------|
| 32 | 67 | 80.7 | 433 | 1 ENOA_TRASC | Q9W711 trachemys s |
| 33 | 67 | 80.7 | 433 | 1 ENOB_CHICK | P07322 gallus gall |
| 34 | 67 | 80.7 | 433 | 1 ENOB_HUMAN | P13929 homo sapien |
| 35 | 67 | 80.7 | 433 | 1 ENOB_MOUSE | P21550 mus musculu |
| 36 | 67 | 80.7 | 433 | 1 ENOB_RABIT | P25704 oryctolagus |
| 37 | 67 | 80.7 | 433 | 1 ENOB_RAT | P15429 rattus norv |
| 38 | 67 | 80.7 | 433 | 1 ENOG_HUMAN | P09104 homo sapien |
| 39 | 67 | 80.7 | 433 | 1 ENOG_MOUSE | P17183 mus musculu |
| 40 | 67 | 80.7 | 433 | 1 ENOG_RAT | P07323 rattus norv |
| 41 | 67 | 80.7 | 433 | 1 ENO_HOMGA | P56252 homarus gam |
| 42 | 67 | 80.7 | 433 | 1 ENO_XENTIA | P08734 xenopus lae |
| 43 | 67 | 80.7 | 433 | 2 Q6PC89 | Q6PC89 brachydantio |
| 44 | 67 | 80.7 | 433 | 2 Q6TH14 | Q6TH14 brachydantio |
| 45 | 67 | 80.7 | 434 | 1 ENO_LOLPE | O02654 loligo peal |

RESULT 1

| | | | | |
|----|--|-----------|------|---------|
| AC | ENOL_HUMAN | STANDARD; | PRT; | 458 AA. |
| DT | 01-FEB-1995 (Rel. 31, Created) | | | |
| DT | 01-FEB-1995 (Rel. 31, Last sequence update) | | | |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) | | | |
| DE | Alpha enolase, lung specific (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neutral enolase) (NME) (Phosphopyruvate hydratase) (HLBI). | | | |
| DE | Name=ENOLB; | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Lung fibroblast; | | | |
| RX | MEDLINE=93372640; PubMed=7689884; | | | |
| RA | Verma M., Kuhl R.N.; | | | |
| RT | "Human lung enolase: cloning and sequencing of cDNA and its inducibility with dexamethasone."; | | | |
| RL | Biochem. Mol. Biol. Int. 30:293-303 (1993). | | | |
| CC | -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O. | | | |
| CC | -1- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer. | | | |
| CC | -1- PATHWAY: Glycolysis. | | | |
| CC | -1- SUBUNIT: Homodimer (By similarity). | | | |
| CC | -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential). | | | |
| CC | -1- INDUCTION: By dexamethasone. | | | |
| CC | -1- SIMILARITY: Belongs to the enolase family. | | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch). | | | |
| CC | EMBL: X66610; CAA47179.1; - | | | |
| DR | PIR: I37360; I37360. | | | |
| DR | HSSP: P56252; 1PDZ. | | | |
| DR | Reactome: Q05524; - | | | |
| DR | MIM: 607098; - | | | |
| DR | GO: 0004634; F:phosphopyruvate hydratase activity; TAS. | | | |
| DR | InterPro: IPR000941; Enolase. | | | |
| DR | Pfam: PF00113; Enolase_C; 1. | | | |
| DR | Pfam: PF03952; Enolase_N; 1. | | | |
| DR | PRINTS: PR00148; ENOLASE. | | | |
| DR | ProDom: PD000902; Enolase; 1. | | | |
| DR | TIGRFAMs: TIGR01060; eno; 1. | | | |
| DR | PROSITE: PS00164; ENOLASE; 1. | | | |

KM Glycolysis; Lyase; Magnesium; Multigene family.
 FT ACT SITE 167 By similarity.
 FT METAL 254 254 Magnesium (By similarity).
 FT METAL 308 308 Magnesium (By similarity).
 FT METAL 336 336 Magnesium (By similarity).
 SQ SEQUENCE 458 AA; 49477 MW; 2590F34A28F4314 CRC64;
 Query Match 91.6%; Score 76; DB 1; Length 458;
 Best Local Similarity 87.5%; Pred. No. 2.7e-05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LVVGLCTQXIKTGAPC 16
 DB 407 LVVGLCTQXIKTGAPC 422
 RESULT 2
 ENOA BOVIN STANDARD; PRT; 433 AA.
 ID ENOA BOVIN STANDARD; PRT; 433 AA.
 AC 09XSJ4;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neutral enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase).
 GN Name=ENO1;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chapman K.L., Newman B., Hillaby M.C., Freemont A.J., Grant M.E., Boot-Handford R., Wallis G.A.;
 RT "Alpha enolase is upregulated in proliferative chondrocytes in the epiphyseal growth plate and in human osteoarthritic tissue.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
 CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer (By similarity).
 CC -1- PATHWAY: Glycolysis.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: Three classes of enolase isoenzymes have been identified in mammalian tissues. Isoenzyme alpha is present in most tissues, beta is localized in muscle tissue, and gamma is found only in nervous tissue.
 CC -1- SIMILARITY: Belongs to the enolase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF149256; AAD33073.1; -.
 DR HSRP; Q9NDH8; IOBP.
 DR InterPro; IPR000941; Enolase.
 DR Pfam; PF00113; Enolase_C_1.
 DR Pfam; PF03952; Enolase_N_1.
 DR PRINTS; PR00148; ENOLASE.
 DR ProDom; PD000902; Enolase; 1.
 DR TIGRfams; TIGR01060; eno; 1.
 KM Glycolysis; Lyase; Magnesium; Multigene family.
 FT INIT MET 0
 FT ACT SITE 157 157 By similarity.
 FT METAL 244 244 Magnesium (By similarity).
 FT METAL 292 292 Magnesium (By similarity).
 FT METAL 317 317 Magnesium (By similarity).

SQ SEQUENCE 433 AA; 47145 MW; B004B365C46F2E0C CRC64;
 Query Match 84.3%; Score 70; DB 1; Length 433;
 Best Local Similarity 81.2%; Pred. No. 0.00033;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTQXIKTGAPC 16
 DB 363 LVVGLCTQXIKTGAPC 398
 RESULT 3
 O804Y6 PRELIMINARY; PRT; 88 AA.
 ID O804Y6 PRELIMINARY; PRT; 88 AA.
 AC O804Y6;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Enolase (Fragment).
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Kim S., Li P., Zheng X., Dunham R.A., Liu Z.;
 RT "Gene expression in the muscles of young and mature channel catfish (Ictalurus punctatus) as analyzed by expressed sequence tags and gene filters.";
 RL Fish Physiol. Biochem. 0:0-0(2003).
 DR EMBL; AF227804; AA025761.1; -.
 DR HSRP; P56252; IEPDZ.
 DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
 DR GO; GO:0004634; P:phosphopyruvate hydratase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR000941; Enolase.
 DR Pfam; PF00113; Enolase_C_1.
 DR ProDom; PD000902; Enolase; 1.
 FT NON_TER 1
 SQ SEQUENCE 88 AA; 9830 MW; 8C14B5B5FDE836C1 CRC64;
 Query Match 80.7%; Score 67; DB 2; Length 88;
 Best Local Similarity 81.2%; Pred. No. 0.00027;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTQXIKTGAPC 16
 DB 38 LVVGLCTQXIKTGAPC 53
 RESULT 4
 Q9NPJ4 PRELIMINARY; PRT; 154 AA.
 ID Q9NPJ4 PRELIMINARY; PRT; 154 AA.
 AC Q9NPJ4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE ENO3, muscle enolase 3 beta (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K., Lehrach H., Pouscka A., Lundberg J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Andreu N., Estivill X., Escarceller M., Sunoy L.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.


```

CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL: AL359213; CAB94588.1; -.
DR HSP: P56252; 1PDI.
DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0000287; F:magnesium ion binding; IEA.
DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO: GO:0006096; P:glycolysis; IEA.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; Enolase_C; 1.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
SQ SEQUENCE 154 AA; 16937 MW; 347B95809B1C864D CRC64;

Query Match 80.7%; Score 67; DB 2; Length 154;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
DB 104 LVVGLCTQIKTGAPC 119

RESULT 5
Q9NG70 PRELIMINARY; PRT; 159 AA.
ID Q9NG70;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2004 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Enolase (Fragment).
OS Peripatus sp. Per3.
OC Eukaryota; Metazoa; Onychophora; Peripatidae; Peripatus.
OC NCBI_TaxId=126380;
RN [1]
RP SEQUENCE FROM N.A.
RA Regier J.C., Shultz J.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL: AF258667; AAF72638.1; -.
DR HSP: P56252; 1PDI.
DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0000287; F:magnesium ion binding; IEA.
DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO: GO:0006096; P:glycolysis; IEA.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; Enolase_C; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
SQ SEQUENCE 159 AA; 17582 MW; 840B266ACD36D3CD CRC64;

Query Match 80.7%; Score 67; DB 2; Length 159;

```

```

Best Local Similarity 81.2%; Pred. No. 0.00046;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
DB 138 LVVGLCTQIKTGAPC 153

RESULT 6
Q96GV1 PRELIMINARY; PRT; 184 AA.
ID Q96GV1;
AC Q96GV1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ENO1 protein (Fragment).
GN Name=ENO1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feringold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rana S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Straubeberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL: BC009218; AA09218.2; -.
DR HSP: P56252; 1PDI.
DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0000287; F:magnesium ion binding; IEA.
DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO: GO:0006096; P:glycolysis; IEA.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; Enolase_C; 1.
DR PROSITE: PS00164; ENOLASE; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
SQ SEQUENCE 184 AA; 20415 MW; F94E113824B5290A CRC64;

```

Query Match 80.7%; Score 67; DB 2; Length 184;
 Best Local Similarity 81.2%; Pred. No. 0.00053;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16
 Db 134 LVVGLCTGQIKTGAPC 149

RESULT 7

ID Q7ZM5 PRELIMINARY; PRT; 259 AA.
 AC Q7ZM5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Enolase (Fragment).
 OS Sparus aurata (Gilthead sea bream).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
 OC Sparidae; Sparus.
 NCBI_TaxID=8175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Ribas L., Mackenzie S., Planas J., Monetti C., Bernardini G., Tort L.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
 CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer (By similarity).
 CC -1- PATHWAY: Glycolysis.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 DR -1- SIMILARITY: Belongs to the enolase family.
 DR EMBL: AY263379; AAO92646.1; -.
 DR HSP: P56252; 1PDZ.
 DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
 DR GO: GO:0016829; F:lyase activity; IEA.
 DR GO: GO:0000287; F:magnesium ion binding; IEA.
 DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.
 DR GO: GO:0006096; F:glycolysis; IEA.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; Enolase_C.1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR GLYCOLYSIS; Lyase; Magnesium.
 FT NON_TER 1
 FT NON_TER 259
 SQ SEQUENCE 259 AA; 28484 MW; 1DB915D3B95531B CRC64;

Query Match 80.7%; Score 67; DB 2; Length 259;
 Best Local Similarity 81.2%; Pred. No. 0.00072;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16
 Db 209 LVVGLCTGQIKTGAPC 224

RESULT 8

ID Q8WU71 PRELIMINARY; PRT; 264 AA.
 AC Q8WU71;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENO1 protein (Fragment).
 GN Name=ENO1;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshynki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gutarra P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]

RN SEQUENCE FROM N.A.
 RP TISSUE=Ovary;
 RC Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
 CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer (By similarity).
 CC -1- PATHWAY: Glycolysis.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the enolase family.
 DR EMBL: BC021166; AAH21166.2; -.
 DR HSP: P56252; 1PDZ.
 DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
 DR GO: GO:0016829; F:lyase activity; IEA.
 DR GO: GO:0000287; F:magnesium ion binding; IEA.
 DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.
 DR GO: GO:0006096; F:glycolysis; IEA.
 DR Pfam: PF00113; Enolase_C.1.
 DR ProDom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR GLYCOLYSIS; Lyase; Magnesium.
 FT NON_TER 1
 FT NON_TER 264
 SQ SEQUENCE 264 AA; 28919 MW; D78A73E001F7685A CRC64;

Query Match 80.7%; Score 67; DB 2; Length 264;
 Best Local Similarity 81.2%; Pred. No. 0.00074;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16
 Db 214 LVVGLCTGQIKTGAPC 229

RESULT 9

ID Q9BT62 PRELIMINARY; PRT; 272 AA.
 AC Q9BT62;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENO1 protein (Fragment).
 GN Name=ENO1;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavari T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pehey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravitski M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 CC Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
 H(2O).
 CC -1- COPACTOR: Magnesium is required for catalysis and for stabilizing
 the dimer (By similarity).
 CC -1- PATHWAY: Glycolysis.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the enolase family.
 DR EMBL; BC004325; AA04325.1; -.
 DR HSSP; P56252; 1P02.
 DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0000287; F:magnesium ion binding; IEA.
 DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR000941; Enolase.
 DR Pfam; PF00113; Enolase_C; 1.
 DR PRINTS; PR00148; ENOLASE.
 DR ProDom; PD000902; Enolase; 1.
 DR PROSITE; PS00164; ENOLASR; 1.
 DR GlycoLysis; Lyase; Magnesium.
 FT NON_TER 1
 SQ SEQUENCE 272 AA; 29883 MW; 08F1755ADEA88DOC CR64;
 Query Match 80.7%; Score 67; DB 2; Length 272;
 Best Local Similarity 81.2%; Pred. No. 0.00076;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTGQIKTGAPC 16
 DB 222 LVVGLCTGQIKTGAPC 237
 RESULT 10
 ID Q71V37 PRELIMINARY; PRT; 336 AA.
 AC Q71V37;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Alpha enolase (Fragment).

OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96207227; PubMed=8619474; DOI=10.1006/abio.1996.0138;
 RA Andersson B., Wenland M.A., Ricatrente J.Y., Liu W., Gibbs R.A.,
 RT "A double adaptor method for improved shotgun library
 construction.";
 RL Anal. Biochem. 236:107-113(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97264341; PubMed=9110174;
 RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
 RA Ricatrente J.Y., Wenland M.A., Lennon G., Gibbs R.A.;
 RT "Large-scale concatenation cDNA sequencing.";
 RL Genome Res. 7:353-358(1997).
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
 H(2O).
 CC -1- COPACTOR: Magnesium is required for catalysis and for stabilizing
 the dimer (By similarity).
 CC -1- PATHWAY: Glycolysis.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the enolase family.
 DR EMBL; AF035286; AAB88178.1; -.
 DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0000287; F:magnesium ion binding; IEA.
 DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR000941; Enolase.
 DR Pfam; PF00113; Enolase_C; 1.
 DR PRINTS; PR00148; ENOLASE.
 DR ProDom; PD000902; Enolase; 1.
 DR PROSITE; PS00164; ENOLASR; 1.
 DR GlycoLysis; Lyase; Magnesium.
 FT NON_TER 1
 SQ SEQUENCE 336 AA; 36308 MW; 2C295E0A28F19301 CR64;
 Query Match 80.7%; Score 67; DB 2; Length 336;
 Best Local Similarity 81.2%; Pred. No. 0.00092;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTGQIKTGAPC 16
 DB 286 LVVGLCTGQIKTGAPC 301
 RESULT 11
 ID Q922A0 PRELIMINARY; PRT; 338 AA.
 AC Q922A0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Enol protein (Fragment).
 GN Name=Eno2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2O).
CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL: BC009018; AA09018.1; -.
DR HSBP; P56252; IPDZ.
DR MGD; MG1:95394; Eno2.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR ProDom; PD000902; Enolase; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR GlycoLysis; Lyase; Magnesium.
FT NON TER 1
SQ SEQUENCE 338 AA; 37146 MW; B0F2F321D7749484 CRC64;

Query Match 80.7%; Score 67; DB 2; Length 338;
Best Local Similarity 81.2%; Pred. No. 0.00092;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 288 LVVGLCTGQIKTGAPC 303

RESULT 12
OGMP2
ID OGMP2 PRELIMINARY; PRT; 341 AA.
AC OGMP2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ENO1 protein.
GN Name=ENO1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2O).
CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL: BC073991; AA73991.1; -.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR00941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR GlycoLysis; Lyase; Magnesium.
FT NON TER 1
SQ SEQUENCE 341 AA; 36928 MW; 96D437CF21772928 CRC64;

Query Match 80.7%; Score 67; DB 2; Length 341;
Best Local Similarity 81.2%; Pred. No. 0.00093;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 291 LVVGLCTGQIKTGAPC 306

RESULT 13
Q99KT7
ID Q99KT7 PRELIMINARY; PRT; 353 AA.
AC Q99KT7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enol protein (Fragment).
GN Name=Enol;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2BCH II; TISSUE=Mammary tumor;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Peltingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RA [2]
RN SEQUENCE FROM N.A.
RP STRAIN=C2ECH II; TISSUE=Mammary tumor;
RC Strausberg R.;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.

DR EMBL; BC004017; AA04017.1; -.
DR HSSP; P56252; 1PDZ.
DR MGI; 95393; Enol.
DR GO; GO:0005515; P:protein binding; TAS.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; Enolase; 1.
DR TIGRPFAM; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR Glycolysis; Lyase; Magnesium.
KW NON TER
SQ SEQUENCE 353 AA; 38299 MW; 2DBD375C81C26A43 CRC64;

Query Match 80.7%; Score 67; DB 2; Length 353;
Best Local Similarity 81.2%; Pred. No. 0.00096;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGXQIKTGAPC 16
DB 303 LVVGLCTGXQIKTGAPC 318

RESULT 14
Q6PHC1 PRELIMINARY; PRT; 366 AA.
ID 06PHC1
AC 06PHC1
DT 05-UTL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Enol protein.
DE Hypothetical protein DKFZp666C036 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Peltingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RA [2]
RN SEQUENCE FROM N.A.
RP STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RC Strausberg R.;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium is required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.

DR EMBL; BC056611; AA056611.1; -.
DR GO; GO:0005515; P:protein binding; TAS.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; Enolase; 1.
DR TIGRPFAM; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
SQ SEQUENCE 366 AA; 39782 MW; 11B90DDDD64B67D1 CRC64;

Query Match 80.7%; Score 67; DB 2; Length 366;
Best Local Similarity 81.2%; Pred. No. 0.00099;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGXQIKTGAPC 16
DB 316 LVVGLCTGXQIKTGAPC 331

RESULT 15
Q658M5 PRELIMINARY; PRT; 374 AA.
ID Q658M5
AC Q658M5
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein DKFZp666C036 (Fragment).
GN Name=DKFZp666C036
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Osaenger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL833741; CAH56247.1; -.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 374 AA; 40512 MW; 681A021B75C43D9 CRC64;
Query Match 80.7%; Score 67; DB 2; Length 374;
Best Local Similarity 81.2%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 LVVGLCTQIKTGAPC 16
Db 324 LVVGLCTQIKTGAPC 339

Search completed: July 13, 2005, 12:13:15
Job time : 58 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 12:06:24 ; Search time 38 Seconds
(without alignments)
43.044 Million cell updates/sec

Title: US-09-647-457E-1

Perfect score: 83
Sequence: 1 LVVGLCTGXQIKTGPAK 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 76 | 91.6 | 458 | 2 I37360 | phosphopyruvate hy |
| 2 | 67 | 80.7 | 395 | 2 I50026 | phosphopyruvate hy |
| 3 | 67 | 80.7 | 433 | 2 A37210 | phosphopyruvate hy |
| 4 | 67 | 80.7 | 434 | 1 NOHUG | phosphopyruvate hy |
| 5 | 67 | 80.7 | 434 | 1 NOMSB | phosphopyruvate hy |
| 6 | 67 | 80.7 | 434 | 1 NOXL | phosphopyruvate hy |
| 7 | 67 | 80.7 | 434 | 2 JC1039 | phosphopyruvate hy |
| 8 | 67 | 80.7 | 434 | 2 JC4186 | phosphopyruvate hy |
| 9 | 67 | 80.7 | 434 | 2 JC4187 | phosphopyruvate hy |
| 10 | 67 | 80.7 | 434 | 2 S06756 | phosphopyruvate hy |
| 11 | 67 | 80.7 | 434 | 2 S10246 | phosphopyruvate hy |
| 12 | 67 | 80.7 | 434 | 2 S10247 | phosphopyruvate hy |
| 13 | 67 | 80.7 | 434 | 2 S02072 | phosphopyruvate hy |
| 14 | 67 | 80.7 | 434 | 2 A29170 | phosphopyruvate hy |
| 15 | 67 | 80.7 | 434 | 2 A32132 | phosphopyruvate hy |
| 16 | 67 | 80.7 | 434 | 2 A24742 | phosphopyruvate hy |
| 17 | 67 | 80.7 | 434 | 2 A23126 | phosphopyruvate hy |
| 18 | 58 | 69.9 | 434 | 2 T25040 | hypothetical prote |
| 19 | 57 | 68.7 | 433 | 2 S07586 | phosphopyruvate hy |
| 20 | 57 | 68.7 | 433 | 2 A23850 | phosphopyruvate hy |
| 21 | 55 | 66.3 | 431 | 2 A53665 | phosphopyruvate hy |
| 22 | 54 | 65.1 | 446 | 2 T03267 | probable phospho |
| 23 | 53 | 63.9 | 326 | 2 JQ1186 | phosphopyruvate hy |
| 24 | 53 | 63.9 | 444 | 2 JQ1185 | phosphopyruvate hy |
| 25 | 53 | 63.9 | 444 | 2 JQ1187 | phosphopyruvate hy |
| 26 | 52 | 62.7 | 445 | 2 T02221 | phosphopyruvate hy |
| 27 | 52 | 62.7 | 445 | 2 S39203 | phosphopyruvate hy |
| 28 | 51 | 61.4 | 444 | 2 T12341 | phosphopyruvate hy |
| 29 | 51 | 61.4 | 446 | 2 S16257 | phosphopyruvate hy |

| | | | | |
|----|------|------|------|----------|
| 30 | 50 | 60.2 | 372 | 2 S24996 |
| 31 | 49 | 59.0 | 446 | 2 S42206 |
| 32 | 48.5 | 58.4 | 437 | 1 NOBY2 |
| 33 | 48.5 | 58.4 | 437 | 1 NOBY2 |
| 34 | 48 | 57.8 | 477 | 2 B96768 |
| 35 | 45 | 54.2 | 456 | 2 S73562 |
| 36 | 44 | 53.0 | 85 | 2 E70531 |
| 37 | 44 | 53.0 | 429 | 2 H83191 |
| 38 | 42 | 50.6 | 433 | 2 H70141 |
| 39 | 41.5 | 50.0 | 440 | 2 S43113 |
| 40 | 41 | 49.4 | 772 | 2 S32659 |
| 41 | 40 | 48.2 | 277 | 2 C82571 |
| 42 | 40 | 48.2 | 475 | 2 G84697 |
| 43 | 39 | 47.0 | 139 | 2 T23371 |
| 44 | 39 | 47.0 | 2054 | 2 T46612 |
| 45 | 39 | 47.0 | 2055 | 2 T30259 |

ALIGNMENTS

RESULT 1
I37360
phosphopyruvate hydratase (EC 4.2.1.11), lung - human
N:Alternate names: enolase
C:Species: Homo sapiens (man)
C:date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I37360; S22071
R:Verma, M.; Kurl, R.N.
Biochem. Int. 30, 293-303, 1993
A:Title: Human lung enolase: cloning and sequencing of cDNA and its inducibility with de
A:Reference number: I37360
A:Accession: I37360
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-458 <VER>
A:Cross-references: UNIPROT:Q05524; EMBL:X66610; NID:g31178; PIDD:CAA47179.1; PIR:g3117;
A>Note: Submitted to the EMBL Data Library, June 1992
C:Function:
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
F:43/Binding site: magnesium 2 (Ser) #status predicted
F:219,364/Active site: Glu, Lys #status predicted
F:254,308,336/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 91.6%; Score 76; DB 2; Length 458;
Best Local Similarity 87.5%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVVGLCTGXQIKTGPAK 16
DB 407 LVVGLCTGXQIKTGPTC 422

RESULT 2
I50026
phosphopyruvate hydratase (EC 4.2.1.11) alpha - American alligator (fragment)
N:Alternate names: alpha-enolase
C:Species: Alligator mississippiensis (American alligator)
C:date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I50026
R:Hedges, S.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 2621-2624, 1994
A:Title: Molecular evidence for the origin of birds
A:Reference number: A53470; M01D:94195794; PMID:8146164
A:Accession: I50026
A:Status: preliminary; nucleic acid sequence not shown; translation not shown; translate
A:Molecule type: mRNA
A:Residues: 1-395 <HED>
A:Cross-references: UNIPROT:P42897; GB:L28078; NID:g472796; PIDD:AAA53671.1; PIR:g472797;
C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 80.7%; Score 67; DB 2; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGXIKTGAPC 16
DB 362 LVVGLCTGXIKTGAPC 377

RESULT 3

A37210 phosphopyruvate hydratase (EC 4.2.1.11) beta - rabbit
N:Alternate names: enolase beta

C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #ext_change 16-Aug-2004
C:Accession: A37210

R:Chin, C.C.O.
J. Protein Chem. 9, 427-432, 1990
A:Title: The primary structure of rabbit muscle enolase.

A:Reference number: A37210; PMID:9113295; PMID:2275753

A:Accession: A37210
A:Status: preliminary
A:Molecule type: protein

A:Residues: 1-433 <CHI>
A:Cross-references: UNIPROT:P25704
C:Superfamily: Enolase
C:Keyword: acetylated amino end; carbon-oxygen lyase; hydro-lyase
F:1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 80.7%; Score 67; DB 2; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGXIKTGAPC 16
DB 383 LVVGLCTGXIKTGAPC 398

RESULT 4

NOHUG phosphopyruvate hydratase (EC 4.2.1.11) gamma - human

N:Alternate names: enolase gamma; neuron-specific enolase
C:Species: *Homo sapiens* (man)

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #ext_change 16-Aug-2004
C:Accession: J00060; S16163; S02077; I56569; S02616; S38303
R:Oliva, D.; Barba, G.; Barbieri, G.; Gallongo, A.; Feo, S.
Gene 79, 355-360, 1989

A:Title: Cloning, expression and sequence homologies of cDNA for human gamma enolase.
A:Reference number: J00060; PMID:9006764; PMID:2792767

A:Accession: J00060
A:Molecule type: mRNA

A:Residues: 1-434 <OLI>

A:Cross-references: UNIPROT:P09104; GB:M22349; NID:9551199; PIDN:AAB59554.1; PID:G182116
R:Oliva, D.; Cali, L.; Feo, S.; Gallongo, A.
Genomics 10, 157-165, 1991
A:Title: Complete structure of the human gene encoding neuron-specific enolase.

A:Reference number: S16163; PMID:91257823; PMID:2045099

A:Accession: S16163
A:Molecule type: DNA

A:Residues: 1-434 <OLI>

A:Cross-references: GB:X51956; NID:931164; PIDN:CAA36215.1; PID:931165
R:McAleese, S.M.; Dunbar, B.; Fothergill, J.E.; Hinks, L.J.; Day, I.N.M.
Eur. J. Biochem. 178, 413-417, 1988

A:Title: Complete amino acid sequence of the neurone-specific gamma isozyme of enolase
A:Reference number: S02077; PMID:89091176; PMID:3308766

A:Accession: S02077
A:Molecule type: mRNA

A:Residues: 2-3, 'Q', 'W', 241-434 <MCA>
A:Cross-references: EMBL:X13120; NID:931145; PIDN:CAA35151.1; PID:9330063

A:Note: part of this sequence was confirmed by protein sequencing
A:Note: 264-Ala and 395-Ala were also found

R:Van Obberghen, E.; Kamholz, J.; Bishop, J.G.

J. Neurosci. Res. 19, 450-456, 1988

A:Title: Human gamma enolase: isolation of a cDNA clone and expression in normal and tumor cells

A:Reference number: I56569; PMID:88259288; PMID:3385803

A:Accession: I56569
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 'GC', 29-126, 'N', 128-434 <VAN>

A:Cross-references: GB:M36768; NID:9182117; PIDN:AAA52388.1; PID:G182118
R:Day, I.N.M.; Allsopp, M.T.E.P.; Moore, D.C.M.; Thompson, R.J.

FEBS Lett. 222, 139-143, 1987
A:Title: Sequence conservation in the 3'-untranslated regions of neurone-specific enolases

A:Reference number: S02616; PMID:88005129; PMID:3653393

A:Accession: S02616
A:Status: not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 425-434 <DAY>

A:Cross-references: GB:Y00691; GB:M27610
R:Harrington, C.R.; Quinn, G.B.; Hurt, J.; Day, I.N.M.; Waschik, C.M.
Biochim. Biophys. Acta 1158, 120-128, 1993

A:Title: Characterisation of an epitope specific to the neuron-specific isoform of human gamma enolase

A:Reference number: S38303; PMID:94002176; PMID:7691181

A:Accession: S38303
A:Molecule type: protein
A:Residues: 156-173 <HAR>

C:Comment: Enolase occurs with at least three isoforms (alpha, beta, and gamma) in mammalian cells. The 191 may be important for the enhanced tolerance to chloride ions of neuroblastoma cells.

A:Gene: GDB:EN02
A:Cross-references: GDB:119872; OMIM:131360

A:Map position: 12p13-12p13
A:Intons: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2; 412/2

C:Complex: homodimer
C:Function: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phosphoenolpyruvate

A:pathway: gluconeogenesis; glycolysis
C:Superfamily: Enolase

C:Keywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolysis; F2-434/Product; phosphopyruvate hydratase gamma #status predicted <WAT>

F2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #status predicted
F210/343/Active site: Glu, Lys #status predicted

F245/293/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 80.7%; Score 67; DB 1; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGXIKTGAPC 16
DB 384 LVVGLCTGXIKTGAPC 399

RESULT 5

NOHUG phosphopyruvate hydratase (EC 4.2.1.11) beta - mouse

N:Alternate names: enolase beta
C:Species: *Mus musculus* (house mouse)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #ext_change 16-Aug-2004
C:Accession: S17109; S18036; S29675; A33921

R:Lamande, N.; Brosset, S.; Keller, A.; Lucas, M.; Lazar, M.
submitted to the EMBL Data Library, September 1991

A:Reference number: S17109

A:Accession: S17109
A:Molecule type: DNA
A:Residues: 1-434 <LAM>

A:Cross-references: UNIPROT:P21550; EMBL:X61600; NID:950848; PIDN:CAA43797.1; PID:950849
R:Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M.

submitted to the EMBL Data Library, October 1991
A:Description: Beta-enolase: a gene expressed in undifferentiated postnatal myoblasts th

A:Reference number: S18036
A:Accession: S18036

A:Molecule type: mRNA
A:Residues: 1-434 <PRT>
A:Cross-references: EMBL:X62667; NID:G50143; PIDN:CAA44540.1; PID:G50144
R:Lazar, M.; Lamande, N.; Broseck, S.; Lucas, M.; Keller, A.
Submitted to the EMBL Data Library, February 1991
A:Reference number: S29675
A:Accession: S29675
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-434 <LAZ>
A:Cross-references: EMBL:X57747; NID:G50846; PIDN:CAA40913.1; PID:G50847
R:Lamande, N.; Mazo, A.M.; Lucas, M.; Montarras, D.; Pinset, C.; Gros, F.; Legault-Demaz
Proc. Natl. Acad. Sci. U.S.A. 86, 4445-4449, 1989
A>Title: Murine muscle-specific enolase: cDNA cloning, sequence, and developmental expre
A:Reference number: A33921; MUID:89282789; PMID:2734257
A:Accession: A33921
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 59-233; 'NA',236-434 <LA2>
A:Cross-references: GB:M20745; NID:G193029; PIDN:AAA37554.1; PID:G387144
A:Experimental source: skeletal muscle
A:Gene: nse
A:Comment: This enzyme is a specific marker protein for the development of nervous syste
C:Keywords: brain; carbon-oxygen lyase; hydro-lyase
C:Superfamily: enolase
A:Pathway: gluconeogenesis; glycolysis
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos
C:Function:
A:Intons: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: Enolase
C:Keywords: carbon-carbon lyase; carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis
P:40/Binding site: magnesium 2 (Ser) #status predicted
P:210,343/Active site: Glu, Lys #status predicted
P:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 80.7%; Score 67; DB 1; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 6
NOX1
phosphopyruvate hydratase (EC 4.2.1.11) ENO1 - African clawed frog
N:Alternate names: enolase ENO1
C:Species: Xenopus laevis (African clawed frog)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Aug-2004
C:Accession: S00463
R:Seg1, N.; Shrutkewski, A.; Dworkin, M.B.; Dworkin-Rae1, E.
Biochem. J. 251, 31-39, 1988
A>Title: Enolase isoenzymes in adult and developing Xenopus laevis and characterization
A:Reference number: S00463; MUID:88268812; PMID:3390159
A:Accession: S00463
A:Molecule type: mRNA
A:Residues: 1-434 <SEG>
A:Cross-references: UNIPROT:P08734; EMBL:Y00718; NID:G66679; PIDN:CAA68706.1; PID:G66680
C:Gene: ENO1
A:Gene: ENO1
C:Function:
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: Enolase
C:Keywords: carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis; hydro-lyase; magnes
P:40/Binding site: magnesium 2 (Ser) #status predicted
P:210,343/Active site: Glu, Lys #status predicted
P:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 80.7%; Score 67; DB 1; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399

Db 384 LVVGLCTGQIKTGAPC 399

RESULT 7
JC1039
phosphopyruvate hydratase (EC 4.2.1.11) - rat
N:Alternate names: neuron-specific enolase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Mar-1993 #sequence_revision 19-Oct-1995 #text_change 03-May-1996
C:Accession: JC1039
R:Zhao, C.; Wang, L.B.; Song, X.W.; Zhang, J.Y.
Chinese Biochem. J. 10, 270-273, 1994
A>Title: cDNA cloning and sequencing of the NSE gene from rat brain.
A:Reference number: JC1039
A:Accession: JC1039
A:Molecule type: mRNA
A:Residues: 1-434 <ZHA>
A:Experimental source: brain, Matar
C:Comment: This enzyme is a specific marker protein for the development of nervous syste
A:Gene: nse
A:Comment: This enzyme is a specific marker protein for the development of nervous syste
C:Keywords: brain; carbon-oxygen lyase; hydro-lyase
C:Superfamily: enolase
A:Pathway: gluconeogenesis; glycolysis
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos
C:Function:
A:Intons: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: Enolase
C:Keywords: carbon-carbon lyase; carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis
P:40/Binding site: magnesium 2 (Ser) #status predicted
P:210,343/Active site: Glu, Lys #status predicted
P:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 9
JC4187
phosphopyruvate hydratase (EC 4.2.1.11) beta chain - chicken
N:Alternate names: beta-2-phospho-D-glycerate hydrolase; enolase
C:Species: Gallus gallus (chicken)
C>Date: 14-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C:Accession: JC4187
R:Tanaka, M.; Maeda, K.; Nakashima, K.
J. Biochem. 117, 554-559, 1995

A>Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phospho
A:Reference number: JCA186; PMID:95355305; PMID:7629021
A:Accession: JCA187
A:Molecule type: mRNA
A:Residues: 1-434 <TAN>
A:Cross-references: UNIPROT:P07322; DDBJ:D37901; NID:G974177; PIDN:BA07133.1; PID:G1616
C:Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported which
rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all the emb
C:Superfamily: enolase
C:Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; phosphoprotein
P1/Modified site: acetylated amino end (Met) #status experimental

Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
DB 384 LVVGLCTQIKTGAPC 399

RESULT 10

phosphopyruvate hydratase (EC 4.2.1.11) beta - human
N:Alternate names: enolase beta; enolase, skeletal muscle; phosphopyruvate hydratase, mu
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
A:Accession: S06756; S14759; S15933; S33330; S08685; S31650
R:Residues: M.; Hinks, L.J.; Day, I.N.M.
Nucleic Acids Res. 17, 8662, 1989

A>Title: Structure of human muscle (beta) enolase mRNA and protein deduced from a genom
A:Reference number: S06756; PMID:90067857; PMID:2587223
A:Accession: S06756
A:Molecule type: mRNA

A:Residues: 1-434 <PES>
A:Cross-references: UNIPROT:P13929; EMBL:X16504; NID:G31169; PIDN:CAA34513.1; PID:G31170
R:Residues: M.; Day, I.N.M.
Biochem. J. 275, 427-433, 1991

A>Title: Molecular structure of the human muscle-specific enolase gene (ENOS).
A:Reference number: S14759; PMID:91222137; PMID:1840492
A:Accession: S14759
A>Status: nucleic acid sequence not shown

A:Residues: 1-434 <PE2>
A:Molecule type: DNA
A:Cross-references: EMBL:X55976
R:Call, L.; Feo, S.; Oliva, D.; Giallongo, A.
Nucleic Acids Res. 18, 1893, 1990

A>Title: Nucleotide sequence of a cDNA encoding the human muscle-specific enolase (MSE).
A:Reference number: S15933; PMID:90245587; PMID:2336366
A:Accession: S15933
A:Molecule type: mRNA

A:Residues: 1-64, 'A', 66-161, 'K', 163-434 <CAL>
A:Cross-references: EMBL:X51957; NID:G34788; PIDN:CAA36216.1; PID:G34789
R:Giallongo, A.; Venturilla, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Feo, S.
Eur. J. Biochem. 214, 367-374, 1993

A>Title: Structural features of the human gene for muscle-specific enolase. Differential
A:Reference number: S33330; PMID:9392497; PMID:5513787
A:Accession: S33330
A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-161, 'K', 163-434 <GTA>
A:Cross-references: EMBL:X56832; NID:G31166; PIDN:CAA40163.1; PID:G31167
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990

C:Genetics:
A:Gene: GDB:ENOS
A:Cross-references: GDB:119873; OMIM:131370
A:Map position: 17pter-17p12
A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle; skele

Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
DB 384 LVVGLCTQIKTGAPC 399

RESULT 11

phosphopyruvate hydratase (EC 4.2.1.11) alpha - mouse
N:Alternate names: 2-phosphoglycerate dehydratase; enolase alpha
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
A:Accession: S10246; A56781
R:Kaghad, M.; Dumont, X.; Chalton, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C

Nucleic Acids Res. 18, 3638, 1990
A>Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.
A:Reference number: S10246; PMID:90301487; PMID:2362815
A:Accession: S10246
A:Molecule type: mRNA

A:Residues: 1-434 <KAG>
A:Cross-references: UNIPROT:P17182; EMBL:X52379; NID:G55490; PIDN:CAA36605.1; PID:G55491
R:Botallico, L.A.; Kendrick, N.C.; Keller, A.; Li, Y.; Tabas, I.
Arterioscler. Thromb. 13, 264-275, 1993

A>Title: Cholesteryl ester loading of mouse peritoneal macrophages is associated with ch
soform.
A:Reference number: A56781; PMID:93152553; PMID:8427861
A:Accession: A56781
A>Status: preliminary

A:Molecule type: protein
A:Residues: 'X', 60, 'X', 62-67, 'X', 69-71, 'XX', 100-109, 'X', 111-112, 'X', 114, 'X', 184-185, 'X',
A:Experimental source: peritoneal macrophages
A:Note: sequence modified after extraction from NCBI backbone
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
DB 384 LVVGLCTQIKTGAPC 399

RESULT 12

phosphopyruvate hydratase (EC 4.2.1.11) gamma - mouse
N:Alternate names: 2-phosphoglycerate dehydratase; enolase gamma
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
A:Accession: S10247
R:Kaghad, M.; Dumont, X.; Chalton, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C

Nucleic Acids Res. 18, 3638, 1990
A>Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.
A:Reference number: S10246; PMID:90301487; PMID:2362815
A:Accession: S10247
A:Molecule type: mRNA

A:Residues: 1-434 <KAG>
A:Cross-references: UNIPROT:P17183; EMBL:X52380; NID:G55494; PIDN:CAA36606.1; PID:G55495
A:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
DB 384 LVVGLCTQIKTGAPC 399

RESULT 13

S02072
phosphopyruvate hydratase (EC 4.2.1.11) beta - rat
N/Alternate names: beta; enolase, muscle-specific
C/Species: Rattus norvegicus (Norway rat)
C/Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C/Accession: S02072
R/Oshima, Y.; Mitsui, H.; Takayama, Y.; Kuehlya, E.; Sakimura, K.; Takahashi, Y.
FEBS Lett. 242, 425-430, 1989
A/Title: cDNA cloning and nucleotide sequence of rat muscle-specific enolase (beta-beta
A/Reference number: S02072; M0ID:8912113; PMID:2914621
A/Accession: S02072
A/Molecule type: mRNA
A/Residues: 1-434 <OH>
A/Cross-references: UNIPROT:P15429; EMBL:Y00979; NID:957781; PIDN:CAA6788.1; PID:957782
A/Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 40-Asp
C/Superfamily: enolase
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle

Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGXQIKTGAPC 16
DB 384 LVVGLCTGXQIKTGAPC 399

RESULT 14
A29170
phosphopyruvate hydratase (EC 4.2.1.11) alpha - human
N/Alternate names: 2-phosphoglycerate dehydratase; enolase 1; enolase alpha
C/Species: Homo sapiens (man)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 16-Aug-2004
C/Accession: S11696; A29170; S52858; A39183
R/Giallongo, A.; Oliva, D.; Cali, L.; Barba, G.; Barbieri, G.; Feo, S.
Eur. J. Biochem. 190, 567-573, 1990
A/Title: Structure of the human gene for alpha-enolase.
A/Reference number: S11696; M0ID:90323004; PMID:2373081
A/Accession: S11696
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-434 <GTA>
A/Cross-references: UNIPROT:P06733; EMBL:X16288; NID:931172; PIDN:CAA4360.1; PID:91678
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1989
R/Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Showe, L.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 6741-6745, 1986
A/Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human alpha
A/Reference number: A29170; M0ID:86313654; PMID:3529090
A/Accession: A29170
A/Molecule type: mRNA
A/Residues: 1-434 <G12>
A/Cross-references: GB:M14328; NID:9182113; PIDN:AA52387.1; PID:9182114
A/Note: the authors translated the codon AAG for residue 193 as His
R/Walter, M.; Leidenberger, F.A.; Schweppe, K.W.; Berg, H.; Northmann, W.
submitted to the EMBL Data Library, February 1995
A/Description: Autoreactive epitopes within the human alpha-enolase and their recognition
A/Reference number: S52858
A/Accession: S52858
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-251, '8', '253-434 <MNL>
A/Cross-references: EMBL:X64907; NID:9693932; PIDN:CAA5931.1; PID:9693933
A/Experimental source: endometrium carcinoma cell line HEC-1B
R/Miles, L.A.; Dahlberg, C.M.; Plescia, J.; Felez, J.; Kato, K.; Plov, E.F.
Biochemistry 30, 1682-1691, 1991
A/Title: Role of cell-surface lysines in plasminogen binding to cells: identification of
A/Reference number: A39183; M0ID:91129243; PMID:1847072
A/Accession: A39183
A/Molecule type: protein
A/Residues: 170-182, 'I', '184', 'R', '186-190; 245-252 <MIL>
C/Genetics:
A/Gene: GDB:ENO1
A/Cross-references: GDB:119871; OMIM:172430

A/Map position: 1p36-1p36
A/Intons: 29/1, 61/1, 80/3, 104/1, 148/3, 223/1, 289/1, 356/2, 392/3, 412/2
A/Function:
A/Description: catalyzes the reversible hydration of phosphoenolpyruvate to 2-phosphogly
C/Superfamily: Enolase
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
P/2-434/Product: phosphopyruvate hydratase alpha #status predicted <MNT>

Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGXQIKTGAPC 16
DB 384 LVVGLCTGXQIKTGAPC 399

RESULT 15
A32132
phosphopyruvate hydratase (EC 4.2.1.11) alpha - duck
N/Alternate names: enolase alpha; tau-crystallin
C/Species: Anas platyrhynchos (domestic duck)
C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 16-Aug-2004
C/Accession: A32132
R/Wistow, G.J.; Lieberman, T.; Williams, L.A.; Stapel, S.O.; de Jong, W.W.; Horwitz, J.; I
J. Cell Biol. 107, 2729-2736, 1988
A/Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens struc
A/Reference number: A92750; M0ID:89079778; PMID:2462567
A/Accession: A32132
A/Molecule type: mRNA
A/Residues: 1-434 <MIS>
A/Cross-references: UNIPROT:P19140; GB:X14195; NID:962455; PIDN:CAA32409.1; PID:962456
C/Superfamily: Enolase
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGXQIKTGAPC 16
DB 384 LVVGLCTGXQIKTGAPC 399

Search completed: July 13, 2005, 12:13:59
Job time : 39 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 12:02:38 ; Search time 160 Seconds

(without alignments)
41.093 Million cell updates/sec

Title: US-09-647-457E-1

Sequence: 1 LVVGLCTQIKTGPACX 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_16Dec04:*

1: Geneseq19808:.*
2: Geneseq19908:.*
3: Geneseq20008:.*
4: Geneseq20018:.*
5: Geneseq20028:.*
6: Geneseq20038:.*
7: Geneseq20048:.*
8: Geneseq20058:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 80 | 96.4 | 16 | AAV43204 | Aay43204 Schizophr |
| 2 | 80 | 96.4 | 17 | AAV43197 | Aay43197 Schizophr |
| 3 | 79 | 95.2 | 16 | AAV43191 | Aay43191 Schizophr |
| 4 | 79 | 95.2 | 17 | AAV43198 | Aay43198 Schizophr |
| 5 | 76 | 91.6 | 458 | ADG79784 | Carbohydr |
| 6 | 76 | 91.6 | 8 | ADG30526 | Pancreas |
| 7 | 67 | 80.7 | 16 | AAV43202 | Aay43202 Schizophr |
| 8 | 67 | 80.7 | 17 | AAV43196 | Aay43196 Schizophr |
| 9 | 67 | 80.7 | 18 | AAV43195 | Aay43195 Schizophr |
| 10 | 67 | 80.7 | 19 | AAV43193 | Aay43193 Schizophr |
| 11 | 67 | 80.7 | 20 | AAV43192 | Aay43192 Schizophr |
| 12 | 67 | 80.7 | 28 | AAV43192 | Aay43192 Schizophr |
| 13 | 67 | 80.7 | 269 | ABU04377 | Human exp |
| 14 | 67 | 80.7 | 272 | ABU04378 | Human exp |
| 15 | 67 | 80.7 | 272 | ABU04375 | Human exp |
| 16 | 67 | 80.7 | 336 | ABU04376 | Human exp |
| 17 | 67 | 80.7 | 420 | AAE38225 | Human exp |
| 18 | 67 | 80.7 | 429 | AAE38225 | Human exp |
| 19 | 67 | 80.7 | 429 | ABU03938 | Human exp |
| 20 | 67 | 80.7 | 433 | AAW14001 | Enolase p |
| 21 | 67 | 80.7 | 433 | AAW14001 | Enolase p |
| 22 | 67 | 80.7 | 433 | ABU03944 | Human exp |
| 23 | 67 | 80.7 | 433 | ABU03942 | Human exp |
| 24 | 67 | 80.7 | 433 | ADG30574 | Pancreas |
| 25 | 67 | 80.7 | 434 | ABE57379 | Rat mucoc |

| | | | | | | |
|----|----|------|-----|---|----------|--------------------|
| 26 | 67 | 80.7 | 434 | 5 | ABP65147 | Abp65147 Hypoxia-r |
| 27 | 67 | 80.7 | 434 | 5 | ABP65155 | Abp65155 Hypoxia-r |
| 28 | 67 | 80.7 | 434 | 5 | AAW48922 | Human eno |
| 29 | 67 | 80.7 | 434 | 6 | ABR64211 | Angiogen |
| 30 | 67 | 80.7 | 434 | 6 | ABR47446 | Breast ca |
| 31 | 67 | 80.7 | 434 | 6 | ABR59704 | Human eno |
| 32 | 67 | 80.7 | 434 | 6 | ABU03929 | Human exp |
| 33 | 67 | 80.7 | 434 | 6 | ABU03943 | Human exp |
| 34 | 67 | 80.7 | 434 | 6 | ABU03934 | Human exp |
| 35 | 67 | 80.7 | 434 | 6 | ABU03936 | Human exp |
| 36 | 67 | 80.7 | 434 | 6 | ABU03935 | Human exp |
| 37 | 67 | 80.7 | 434 | 6 | ABU03932 | Human exp |
| 38 | 67 | 80.7 | 434 | 6 | ABU03930 | Human exp |
| 39 | 67 | 80.7 | 434 | 6 | ABU03931 | Human exp |
| 40 | 67 | 80.7 | 434 | 6 | ABU03937 | Human exp |
| 41 | 67 | 80.7 | 434 | 6 | ABU03933 | Human exp |
| 42 | 67 | 80.7 | 434 | 6 | ABM04797 | Human alp |
| 43 | 67 | 80.7 | 434 | 7 | ADB85166 | Rat enola |
| 44 | 67 | 80.7 | 434 | 7 | ADC52079 | Human alp |
| 45 | 67 | 80.7 | 434 | 7 | ADD27706 | Human adl |

ALIGNMENTS

| | | |
|----------|---|---------------------------|
| RESULT 1 | AAV43204 | standard; peptide; 16 AA. |
| ID | AAV43204 | |
| XX | AAV43204; | |
| AC | 11-UMN-2000 (first entry) | |
| DT | Schizophrenic derived antibody binding epitope #14. | |
| XX | Schizophrenic derived antibody; binding epitope; schizophrenia; | |
| KW | platelet-associated antibody; diagnosis. | |
| KM | Synthetic. | |
| OS | MO9951725-A2. | |
| XX | 14-OCT-1999. | |
| PD | 30-MAR-1999; 99WO-IL000190. | |
| PF | 02-APR-1998; 98IL-00123925. | |
| XX | (YEDA) YEDA RES & DEV CO LTD. | |
| PA | Shintzky M, Deckmann M; | |
| PI | WPI; 1999-611037/52. | |
| DR | New peptides useful for diagnosis of schizophrenia. | |
| PT | Claim 4; Page 21; 37pp; English. | |
| PS | This sequence is a peptide of the invention, which binds antibodies found | |
| XX | in elevated levels in body fluids of schizophrenic patients. The peptide | |
| CC | is useful in an assay for the diagnosis of schizophrenia, by binding the | |
| CC | peptide to a platelet-containing fraction of blood, or a fraction | |
| CC | containing platelet-associated antibodies (PAA) shed from the platelets, | |
| CC | or preferably whole blood. The new peptides are able to differentiate | |
| CC | between plasma samples from schizophrenic and non-schizophrenic patients, | |
| CC | and can do so without having to first isolate the platelet-associated | |
| CC | antibodies (PAA) fraction | |
| XX | Sequence 16 AA; | |
| SQ | Query Match 96.4%; Score 80; DB 2; Length 16; | |
| | Best Local Similarity 93.8%; Pred. No. 8.2e-06; | |
| | Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | |

OY 1 LVVGLCTQIKTGPAC 16
 |||||
 Db 1 LVVGLCTQIKTGPAC 16

RESULT 2
 AAY43197
 ID AAY43197 standard; peptide; 17 AA.

AC AAY43197;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #7.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shintzky M, Deckmann M;

DR WPI; 1999-611037/52.

PS New peptides useful for diagnosis of schizophrenia.

PS Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction

SQ Sequence 17 AA;

Query Match 96.4%; Score 80; DB 2; Length 17;
 Best Local Similarity 93.8%; Pred. No. 8.7e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVVGLCTQIKTGPAC 16
 |||||
 Db 1 LVVGLCTQIKTGPAC 16

RESULT 3
 AAY43191

ID AAY43191 standard; peptide; 16 AA.

AC AAY43191;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #1.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 platelet-associated antibody; diagnosis.

XX

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shintzky M, Deckmann M;

DR WPI; 1999-611037/52.

PS New peptides useful for diagnosis of schizophrenia.

PS Claim 2; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction

SQ Sequence 16 AA;

Query Match 95.2%; Score 79; DB 2; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.2e-05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVVGLCTQIKTGPAC 16
 |||||
 Db 1 LVVGLCTQIKTGPAC 16

RESULT 4
 AAY43198

ID AAY43198 standard; peptide; 17 AA.

AC AAY43198;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #8.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shintzky M, Deckmann M;

DR WPI; 1999-611037/52.

PS New peptides useful for diagnosis of schizophrenia.

PS Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction
 XX
 SQ Sequence 17 AA;
 Query Match 95.2%; Score 79; DB 2; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LVVGLCTQXKTGPAC 16
 Db 1 LVVGLCTQXKTGPAC 16
 RESULT 5
 ID AAG79784 standard; protein; 458 AA.
 XX AAG79784;
 AC
 XX 16-APR-2003 (first entry)
 DT
 XX
 DE Carbohydrate-associated protein (CHOP) -6.
 XX
 KW Human; carbohydrate associated polypeptides; CHOP; cancer;
 KW carbohydrate metabolism; diabetes; anaemia; hypoglycaemia; obesity;
 KW glycogen storage disease; neurological dysfunction; gene therapy;
 KW cell proliferation; actinic keratosis; arteriosclerosis; inflammation;
 KW atherosclerosis; cirrhosis; hepatitis; psoriasis; autoimmune disorder;
 KW acquired immunodeficiency syndrome; AIDS; humanized; transgenic;
 KW Addison's disease; allergy; asthma; contact dermatitis; bronchitis; gout;
 KW Hashimoto's thyroiditis; infection; reproduction; endometriosis;
 KW polycystic ovary syndrome; ovarian hyperstimulation syndrome;
 KW Down syndrome; cystic fibrosis; sickle cell anaemia; thalassemia;
 KW myocarditis; cardiomyopathy; Alzheimer's disease; Parkinson's disease;
 KW dementia; depression; epilepsy; Tourette's disorder; schizophrenia;
 KW central nervous system; cerebral palsy; mood; anxiety; knockin.
 OS
 XX Homo sapiens.
 FH
 XX
 FT Key Location/Qualifiers
 FT Peptide 1..455
 FT /label= Enolase
 FT /note= "Identified by BLAST_DOMO"
 FT Peptide 1..293
 FT /label= Enolase lyase
 FT /note= "Identified by BLAST_PRODOM"
 FT Peptide 2..456
 FT /label= Enolase
 FT /note= "Identified by HMWER_PFAW"
 FT Peptide 2..456
 FT /label= Enolase
 FT /note= "Identified by BLAST_DOMO"
 FT Peptide 7..456
 FT /label= Enolase
 FT /note= "Identified by BLAST_DOMO"
 FT Peptide 35..57
 FT /label= Enolase protein
 FT /note= "Identified by BLIMPS_BLOCKS"
 FT Peptide 38..52
 FT /label= Enolase signature
 FT /note= "Identified by BLIMPS_PRINTS"
 FT Peptide 113..129
 FT /label= Enolase signature
 FT /note= "Identified by BLIMPS_PRINTS"

FT Protein 153..202
 FT /label= Enolase protein
 FT /note= "Identified by BLIMPS_BLOCKS"
 FT Peptide 173..186
 FT /label= Enolase signature
 FT /note= "Identified by BLIMPS_PRINTS"
 FT Protein 229..271
 FT /label= Enolase protein
 FT /note= "Identified by BLIMPS_BLOCKS"
 FT Peptide 275..440
 FT /label= Lyase magnesium enolase
 FT /note= "Identified by BLAST_PRODOM"
 FT Protein 302..316
 FT /label= Enolase protein
 FT /note= "Identified by BLIMPS_BLOCKS"
 FT Peptide 314..362
 FT /label= Enolase signature
 FT /note= "Identified by PROFILESKAN"
 FT Protein 331..366
 FT /label= Enolase protein
 FT /note= "Identified by BLIMPS_BLOCKS"
 FT Peptide 335..346
 FT /label= Enolase signature
 FT /note= "Identified by BLIMPS_PRINTS"
 FT Peptide 361..375
 FT /label= Enolase signature
 FT /note= "Identified by BLIMPS_PRINTS"
 FT Peptide 392..409
 FT /label= Enolase signature
 FT /note= "Identified by BLIMPS_PRINTS"
 FT Protein 403..441
 FT /label= Enolase protein
 FT /note= "Identified by BLIMPS_BLOCKS"
 FT Peptide 408..456
 FT /label= Enolase lyase glycolysis
 FT /note= "Identified by BLAST_PRODOM"
 XX
 PN MO200297060-A2.
 XX
 PD 05-DEC-2002.
 XX
 XX 22-MAY-2002; 2002WC-US018354.
 XX
 PR 25-MAY-2001; 2001US-0293768P.
 PR 01-AUG-2001; 2001US-0309548P.
 PR 23-AUG-2001; 2001US-0314400P.
 PR 19-OCT-2001; 2001US-0343706P.
 PR 07-DEC-2001; 2001US-0337999P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Swarnakar A, Gorvad AE, Hafalia AJA, Duggan BM, Emerling BM;
 PI Ison CH, Nguyen DB, Lee EA, Yue H, Foraythe ID, Li JK;
 PI Thangavelu K, Walla NK, Burford N, Mason PM, Lal PG, Lee S;
 PI Becha SD, Tang YT;
 XX
 DR WPI; 2003-140462/13.
 DR N-PSDB; ABA00836.
 XX
 PT Novel human carbohydrate associated polypeptide, useful in diagnosis,
 PT treatment and prevention of carbohydrate metabolism, cell proliferative,
 PT autoimmune/inflammatory, reproductive, and neurological disorders.
 XX
 PS Claim 1; Page 129-30; 141pp; English.
 XX
 CC The sequences given in AAG79779-88 represent human carbohydrate
 CC associated polypeptides (CHOP). The CHOP polypeptides and the nucleotide
 CC sequences encoding them, are useful for diagnosing, treating and
 CC preventing cancer, carbohydrate metabolic disorders (e.g. diabetes,
 CC anaemia, hypoglycaemia, obesity, glycogen storage disease, neurological
 CC dysfunctions), cell proliferative disorders (e.g. actinic keratosis,
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis),
 CC autoimmune/inflammatory disorders (such as acquired immunodeficiency

CC syndrome (AIDS), Addison's disease, allergies, asthma, contact
CC dermatitis, bronchitis, gout, Hashimoto's thyroiditis), viral, bacterial,
CC fungal, parasitic, protozoal and helminthic infections, reproductive
CC disorders (e.g. endometriosis, polycystic ovary syndrome, ovarian
CC hyperstimulation syndrome), genetic disorders (e.g. Down syndrome, cystic
CC fibrosis, sickle cell anemia, thalassemia), cardiac disorders (e.g.
CC myocarditis, cardiomyopathy), neurological disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, dementia, depression, epilepsy, Tourette's
CC disorder, schizophrenia), and developmental disorders of central nervous
CC system (e.g. cerebral palsy), mental disorders (e.g. mood, anxiety). CHOP
CC proteins are useful in a number of drug screening techniques, and to
CC analyse the proteome of a tissue or cell type. CHOP cDNA is useful for
CC creating "knockin" humanized animals or transgenic animals to model human
CC diseases, in somatic or germline gene therapy, to generate a transcript
CC image of a tissue or cell type, for detecting differences in the
CC chromosomal location due to translocation, inversion, etc., among normal,
CC carrier or affected individuals, and as hybridization probes for mapping
CC naturally occurring genomic sequences
SQ Sequence 458 AA;

Query Match 91.6%; Score 76; DB 6; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.0008;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVVGLCTQXQIKTGPAC 16
| | | | | | | | | | | | | | | | | |
DB 407 LVVGLCTQXQIKTGPAC 422

RESULT 6
ADQ30526
ID ADQ30526 standard; protein; 458 AA.

XX ADQ30526;

DT 23-SBP-2004 (first entry)

XX Pancreas cancer marker - alpha enolase.

XX cytostatic; diagnosis; pancreatic cancer; antibody; antisense construct;

KM differential expression.

XX Homo sapiens.

PN MO2004055519-A2.

PD 01-JUL-2004.

PF 11-DEC-2003; 2003WO-EP014057.

XX 17-DEC-2002; 2002EP-00028058.

PR 05-NOV-2003; 2003EP-00025237.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.

PI Chen J, Hu L, Liu TH, Lu ZH, Shen Y;

DR WPI; 2004-488121/46.

PT New specific markers comprises at least one polypeptide up-regulated in
PT pancreatic cancer, useful for diagnosing pancreatic cancer.

PS Claim 1; SEQ ID NO 13; 381bp; English.

CC The invention relates to a marker (I) for diagnosis of pancreatic cancer
CC comprising at least one polypeptide selected from 55 proteins up-
CC regulated in pancreatic cancer (Table 2 and Table 3, given in the
CC specification) or from 68 proteins with higher levels in pancreatic
CC cancer compared to normal tissue (Table 6, given in the specification).
CC (I) is a polypeptide for use as a marker or as a component of a marker
CC for diagnosis of pancreatic cancer and/or the susceptibility to

CC pancreatic cancer. A compound (antibody, an antibody-derivative, an
CC antibody fragment, a peptide, or an antisense construct) identified by
CC screening methods using (I) is useful for treatment or prevention of
CC pancreatic cancer. It is also useful for the preparation of a diagnostic
CC composition for diagnosing pancreatic cancer or a predisposition for
CC pancreatic cancer. The current polypeptides were found to be
CC differentially expressed in pancreatic tissue obtained from individuals
CC suffering from pancreatic cancer as compared to healthy pancreatic
CC tissue. They have been identified as suitable as markers of pancreatic
CC cancer for early diagnosis of the disease. This sequence corresponds to a
CC protein marker of the invention.

Query Match 91.6%; Score 76; DB 8; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.0008;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVVGLCTQXQIKTGPAC 16
| | | | | | | | | | | | | | | | | |
DB 407 LVVGLCTQXQIKTGPAC 422

RESULT 7
AAV43202
ID AAV43202 standard; peptide; 16 AA.

XX AAV43202;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #12.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;

KM platelet-associated antibody; diagnosis.

XX Synthetic.

PN MO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

XX 02-APR-1998; 98IL-00123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.

PS Claim 4; Page 21; 37bp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction

SQ Sequence 16 AA;

Query Match 80.7%; Score 67; DB 2; Length 16;
Best Local Similarity 81.2%; Pred. No. 0.00099;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQXQIKTGPAC 16

Db 1 LVVGLCTGQIKTGAPC 16

RESULT 8

AAV43196

ID AAV43196 standard; peptide; 17 AA.

XX AAV43196;

XX 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #6.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
XX platelet-associated antibody; diagnosis.

XX Synthetic.

XX WO951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL000190.

XX 02-APR-1998; 98IL-00123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shintzky M, Deckmann M;

XX MPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia.

XX Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction

SQ Sequence 17 AA;

Query Match 80.7%; Score 67; DB 2; Length 17;
Best Local Similarity 81.2%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

Db 1 LVVGLCTGQIKTGAPC 16

RESULT 9

AAV43195

ID AAV43195 standard; peptide; 18 AA.

XX AAV43195;

XX 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #5.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
XX platelet-associated antibody; diagnosis.

XX Synthetic.

PN WO951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL000190.

XX 02-APR-1998; 98IL-00123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shintzky M, Deckmann M;

XX MPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia.

XX Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction

SQ Sequence 18 AA;

Query Match 80.7%; Score 67; DB 2; Length 18;
Best Local Similarity 81.2%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

Db 2 LVVGLCTGQIKTGAPC 17

RESULT 10

AAV43194

ID AAV43194 standard; peptide; 19 AA.

XX AAV43194;

XX 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #4.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
XX platelet-associated antibody; diagnosis.

XX Synthetic.

XX WO951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL000190.

XX 02-APR-1998; 98IL-00123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shintzky M, Deckmann M;

XX MPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia.
XX Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found

CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction
 XX
 SQ Sequence 19 AA;

Query Match 80.7%; Score 67; DB 2; Length 19;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
 DB 3 LVVGLCTQIKTGAPC 18

RESULT 11
 AAY43193
 ID AAY43193 standard; peptide; 20 AA.

AC AAY43193;
 XX
 DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #3.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.

XX Synthetic.

OS
 XX WO9951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL000190.

XX 02-APR-1998; 98IL-00123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

XX WPI, 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia.

XX Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction
 XX

SQ Sequence 20 AA;

Query Match 80.7%; Score 67; DB 2; Length 20;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
 DB 4 LVVGLCTQIKTGAPC 19

RESULT 12
 AAY43192
 ID AAY43192 standard; peptide; 28 AA.

AC AAY43192;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #2.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.

XX Synthetic.

OS
 XX WO9951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL000190.

XX 02-APR-1998; 98IL-00123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

XX WPI, 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia.

XX Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction
 XX

SQ Sequence 28 AA;

Query Match 80.7%; Score 67; DB 2; Length 28;
 Best Local Similarity 81.2%; Pred. No. 0.0017;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
 DB 12 LVVGLCTQIKTGAPC 27

RESULT 13
 ABU04377
 ID ABU04377 standard; protein; 269 AA.

XX ABU04377;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1043.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 XX protease; protease inhibitor; transporter; cytoskeletal protein;
 XX receptor; transcription factor; cancer; MHC;
 XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.

PN W0200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WC-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
PI
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1043; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC creating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 269 AA;
XX
XX Query Match 80.7%; Score 67; DB 6; Length 269;
XX Best Local Similarity 81.2%; Pred. No. 0.014;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 LVVGLCTGQIKTGAPC 16
DB 219 LVVGLCTGQIKTGAPC 234

RESULT 14
ABU04378
ID ABU04378 standard; protein; 272 AA.
XX
XX ABU04378;
AC
XX
DT 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1044.
DE
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
OS
XX

PN W0200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WC-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
PI
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1044; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC creating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 272 AA;
XX
XX Query Match 80.7%; Score 67; DB 6; Length 272;
XX Best Local Similarity 81.2%; Pred. No. 0.014;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 LVVGLCTGQIKTGAPC 16
DB 222 LVVGLCTGQIKTGAPC 237

RESULT 15
ABU04375
ID ABU04375 standard; protein; 272 AA.
XX
XX ABU04375;
AC
XX
DT 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1041.
DE
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
OS
XX

```

PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicx RM, Tomlinson AL, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1041; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 272 AA;

```

```

Query Match      80.7%; Score 67; DB 6; Length 272;
Best Local Similarity 81.2%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 LVVGLCTXQIKTGPAC 16
   |||||
Db 222 LVVGLCTGQIKTGAPC 237

```

Search completed: July 13, 2005, 12:12:13
Job time : 162 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using bw model

Run on: July 13, 2005, 12:06:44 ; Search time 41 Seconds
(without alignments)
30.952 Million cell updates/sec

Title: US-09-647-457E-1

Perfect score: 83

Sequence: 1 LVVGLCTQIKTGAPAC 17

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA:*
- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
 - 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
 - 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
 - 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
 - 5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
 - 6: /cgn2_6/prodata/1/1aa/backfillset1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------------------|--------------------|
| 1 | 67 | 80.7 | 434 | 4 US-09-949-016-6153 | Sequence 6153, Ap |
| 2 | 67 | 80.7 | 443 | 4 US-09-949-016-8359 | Sequence 8359, Ap |
| 3 | 44 | 53.0 | 444 | 4 US-09-352-991A-21020 | Sequence 21020, A |
| 4 | 44 | 53.0 | 444 | 4 US-09-328-352-7269 | Sequence 7269, Ap |
| 5 | 44 | 53.0 | 445 | 4 US-09-540-236-2354 | Sequence 2354, Ap |
| 6 | 38.5 | 46.4 | 148 | 4 US-09-248-796A-17054 | Sequence 17054, A |
| 7 | 38 | 45.8 | 37 | 2 US-08-248-839C-65 | Sequence 65, Appl |
| 8 | 38 | 45.8 | 233 | 4 US-09-216-393B-110 | Sequence 110, Appl |
| 9 | 38 | 45.8 | 511 | 3 US-09-105-039A-2 | Sequence 2, Appl1 |
| 10 | 38 | 45.8 | 530 | 3 US-09-105-039A-4 | Sequence 4, Appl1 |
| 11 | 37.5 | 45.2 | 66 | 4 US-09-248-796A-22813 | Sequence 22813, A |
| 12 | 37 | 44.6 | 127 | 4 US-09-711-164-348 | Sequence 348, App |
| 13 | 37 | 44.6 | 456 | 4 US-09-543-681A-6090 | Sequence 6090, Ap |
| 14 | 37 | 44.6 | 459 | 4 US-09-489-039A-10061 | Sequence 10061, A |
| 15 | 37 | 44.6 | 670 | 4 US-09-575-081B-24 | Sequence 24, Appl |
| 16 | 37 | 44.6 | 670 | 4 US-09-575-081B-26 | Sequence 26, Appl |
| 17 | 37 | 44.6 | 1886 | 3 US-08-538-105-3 | Sequence 3, Appl1 |
| 18 | 36 | 43.4 | 12 | 4 US-09-417-608A-55 | Sequence 55, Appl |
| 19 | 36 | 43.4 | 63 | 4 US-08-469-260A-431 | Sequence 431, App |
| 20 | 36 | 43.4 | 63 | 4 US-08-488-446-431 | Sequence 431, App |
| 21 | 36 | 43.4 | 63 | 4 US-08-467-344A-431 | Sequence 431, App |
| 22 | 36 | 43.4 | 63 | 4 US-08-424-550B-431 | Sequence 431, App |
| 23 | 36 | 43.4 | 108 | 4 US-09-328-352-5857 | Sequence 5857, App |
| 24 | 36 | 43.4 | 139 | 4 US-09-902-540-14334 | Sequence 14334, A |
| 25 | 36 | 43.4 | 211 | 4 US-09-270-767-36404 | Sequence 36404, A |
| 26 | 36 | 43.4 | 211 | 4 US-09-270-767-51621 | Sequence 51621, A |
| 27 | 36 | 43.4 | 238 | 4 US-09-252-991A-24386 | Sequence 24386, A |

| | | | | | |
|----|----|------|-----|------------------------|--------------------|
| 28 | 36 | 43.4 | 305 | 4 US-09-902-540-14722 | Sequence 14722, A |
| 29 | 36 | 43.4 | 470 | 2 US-08-959-011-1 | Sequence 1, Appl1 |
| 30 | 35 | 42.2 | 45 | 1 US-07-973-852-1 | Sequence 1, Appl1 |
| 31 | 35 | 42.2 | 45 | 1 US-07-950-773-1 | Sequence 1, Appl1 |
| 32 | 35 | 42.2 | 46 | 4 US-09-030-619-230 | Sequence 230, App |
| 33 | 35 | 42.2 | 58 | 3 US-08-676-124-73 | Sequence 73, Appl |
| 34 | 35 | 42.2 | 58 | 3 US-09-414-878-73 | Sequence 73, Appl |
| 35 | 35 | 42.2 | 58 | 3 US-09-240-136-73 | Sequence 73, Appl |
| 36 | 35 | 42.2 | 58 | 4 US-09-638-770A-73 | Sequence 73, Appl |
| 37 | 35 | 42.2 | 148 | 4 US-09-134-000C-5009 | Sequence 5009, App |
| 38 | 35 | 42.2 | 218 | 4 US-09-673-395A-249 | Sequence 249, App |
| 39 | 35 | 42.2 | 262 | 4 US-09-252-991A-25231 | Sequence 25231, A |
| 40 | 35 | 42.2 | 281 | 1 US-07-941-523-23 | Sequence 23, Appl |
| 41 | 35 | 42.2 | 282 | 3 US-09-134-001C-5083 | Sequence 5083, App |
| 42 | 35 | 42.2 | 296 | 1 US-08-320-161-11 | Sequence 11, Appl |
| 43 | 35 | 42.2 | 296 | 1 US-08-137-175A-3 | Sequence 3, Appl1 |
| 44 | 35 | 42.2 | 296 | 3 US-08-479-017-3 | Sequence 3, Appl1 |
| 45 | 35 | 42.2 | 296 | 3 US-08-455-829-11 | Sequence 11, Appl |

ALIGNMENTS

RESULT 1
US-09-949-016-6153
Sequence 6153, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6153
LENGTH: 434
TYPE: PRT
ORGANISM: Human
US-09-949-016-6153
Query Match 80.7%; Score 67; DB 4; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB 1 LVVGLCTQIKTGAPAC 16
384 LVVGLCTQIKTGAPC 399
RESULT 2
US-09-949-016-8359
Sequence 8359, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8359
LENGTH: 443
TYPE: PRT
ORGANISM: Human
US-09-949-016-8359

Query Match
Best Local Similarity 80.7%; Score 67; DB 4; Length 443;
81.2%; Pred. No. 0.0056;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQXIKTGAPAC 16
| | | | | | | | | | | | | | | | | |
Db 393 LVVGLCTQXIKTGAPC 408

RESULT 3
US-09-252-991A-21020
Sequence 21020, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21020
TYPE: PRT
LENGTH: 444
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21020

Query Match
Best Local Similarity 53.0%; Score 44; DB 4; Length 444;
56.2%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 LVVGLCTQXIKTGAPAC 16
| | | | | | | | | | | | | | | | | |
Db 397 LAVGTAAQIKTGSLC 412

RESULT 4
US-09-328-352-7269
Sequence 7269, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7269
LENGTH: 444
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-7269

Query Match
Best Local Similarity 53.0%; Score 44; DB 4; Length 444;
56.2%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 LVVGLCTQXIKTGAPAC 16
| | | | | | | | | | | | | | | | | |

Db 397 LAVGTAAQIKTGSLC 412

RESULT 5
US-09-540-236-2354
Sequence 2354, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2354
LENGTH: 445
TYPE: PRT
ORGANISM: M.catarhalis
US-09-540-236-2354

Query Match
Best Local Similarity 53.0%; Score 44; DB 4; Length 445;
56.2%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 LVVGLCTQXIKTGAPAC 16
| | | | | | | | | | | | | | | | | |
Db 397 LAVGTAAQIKTGSLC 412

RESULT 6
US-09-248-796A-17054
Sequence 17054, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17054
LENGTH: 148
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-17054

Query Match
Best Local Similarity 46.4%; Score 38.5; DB 4; Length 148;
68.8%; Pred. No. 68;
Matches 11; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 LVVGLCTQXIKTG-PA 15
| | | | | | | | | | | | | | | | | |
Db 98 LSVGRSQIKTGAPA 113

RESULT 7
US-08-248-839C-65
Sequence 65, Application US/08248839C
Patent No. 5843702
GENERAL INFORMATION:
APPLICANT: McConnell, David
APPLICANT: Devine, Kevin
APPLICANT: O'Kane, Charles
TITLE OF INVENTION: A Gene Expression System
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESS: No. 58437020 No. 5843702disk of No. 5843702th America, Inc.

```
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,839C
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 3614.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-248-839C-65

Query Match
Best Local Similarity 45.8%; Score 38; DB 2; Length 37;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GLCTQIKTGPAC 16
DB 18 GLCDLWKRRGPGC 30

RESULT 8
US-09-216-393B-110
; Sequence 110, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-110

Query Match
Best Local Similarity 45.8%; Score 38; DB 4; Length 233;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LCTQIKTGPAC 16
DB 3 VCECKKTGPGC 14

RESULT 9
US-09-105-039A-2
; Sequence 2, Application US/09105039A
; Patent No. 6001806
; GENERAL INFORMATION:
```

```
APPLICANT: Hilbert, David M.
APPLICANT: Bednarek, Daniel P.
APPLICANT: Nardelli, Bernardetta
APPLICANT: Murphy, Marianne
APPLICANT: Parmelee, David
APPLICANT: Gronowski, Ann
APPLICANT: Schreiber, Robert
TITLE OF INVENTION: Interferon Stimulating Protein and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,039A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB384
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-039A-2

Query Match
Best Local Similarity 45.8%; Score 38; DB 3; Length 511;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTXQIKTGP 14
DB 24 CNAQMKTGP 32

RESULT 10
US-09-105-039A-4
; Sequence 4, Application US/09105039A
; Patent No. 6001806
; GENERAL INFORMATION:
; APPLICANT: Hilbert, David M.
; APPLICANT: Bednarek, Daniel P.
; APPLICANT: Nardelli, Bernardetta
; APPLICANT: Murphy, Marianne
; APPLICANT: Parmelee, David
; APPLICANT: Gronowski, Ann
; APPLICANT: Schreiber, Robert
TITLE OF INVENTION: Interferon Stimulating Protein and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
```

```
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,039A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB384
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-039A-4
```

```
Query Match          45.8%; Score 38; DB 3; Length 530;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      6 CTXQIKTGP 14
      |||:|:|
Db      42 CNAQMKTGP 50
```

```
RESULT 11
US-09-248-796A-22813
Sequence 22813, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22813
LENGTH: 66
TYPE: PRT
ORGANISM: Candida albicans
FEATURES:
NAME/KEY: UNSURE
LOCATION: (30)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknc
US-09-248-796A-22813
```

```
Query Match          45.2%; Score 37.5; DB 4; Length 66;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 8; Conservative 2; Mismatches 1; Indels 5; Gaps 1;
```

```
QY      3 VGLCTXQ-----IKTG 13
      :|:|:|:|
Db      48 IGLCTIOSAMISVKTG 63
```

```
RESULT 12
US-09-711-164-348
Sequence 348, Application US/09711164
Patent No. 6589738
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Karl
APPLICANT: Zyking, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
FILE REFERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 348
LENGTH: 127
TYPE: PRT
ORGANISM: Escherichia coli
US-09-711-164-348
```

```
Query Match          44.6%; Score 37; DB 4; Length 127;
Best Local Similarity 46.2%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      4 GLCTYQIKTGPAC 16
      |||:|:|
Db      33 GLITSKVKSRPQC 45
```

```
RESULT 13
US-09-543-681A-6090
Sequence 6090, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6090
LENGTH: 456
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-6090
```

```
Query Match          44.6%; Score 37; DB 4; Length 456;
Best Local Similarity 61.5%; Pred. No. 3.4e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 LVGLCTYQIKTG 13
      |||:|:|
Db      407 LAVGTPAQIKTG 419
```

```
RESULT 14
US-09-489-039A-10061
Sequence 10061, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
```


; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 10061
 ; LENGTH: 459
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-10061

Query Match 44.6%; Score 37; DB 4; Length 459;
 Best Local Similarity 61.5%; Pred. No. 3.4e+02;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTXQIKTG 13
 DB 410 LAVGTAAQIKTG 422

RESULT 15
 US-09-575-081B-24
 ; Sequence 24, Application US/09575081B
 ; Patent No. 6692934
 ; GENERAL INFORMATION:
 ; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
 ; TITLE OF INVENTION: NOVEL ORGANIC ANION TRANSPORT PROTEINS
 ; FILE REFERENCE: DB23
 ; CURRENT APPLICATION NUMBER: US/09/575,081B
 ; CURRENT FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: 60/135,081
 ; PRIOR FILING DATE: 1999-05-20
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 24
 ; LENGTH: 670
 ; TYPE: PRT
 ; ORGANISM: Rat
 US-09-575-081B-24

Query Match 44.6%; Score 37; DB 4; Length 670;
 Best Local Similarity 53.3%; Pred. No. 4.9e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 2 VVGLCTXQIKTG 16
 DB 496 VVGLC---KKGPEC 506

Search completed: July 13, 2005, 12:14:47
 Job time : 43 secs

This Page Blank (uspto)

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

This Page Blank (uspto)